

Q1750.1765  
Adonis

09/535364

L3 ANSWER 9 OF 15 MEDLINE DUPLICATE 7  
AB The large number of protein consensus sequences that may be recognized without computer analysis are **reviewed**. These include the extensive range of known phosphorylation site **motifs** for protein **kinases**; metal binding sites for calcium, zinc, copper, and iron; enzyme active site motifs; nucleotide binding and covalent attachment sites for prosthetic groups, carbohydrate, and lipids. Of particular notes is the increasing realization of the importance for cellular regulation of protein-protein interaction motifs and sequences that target proteins to particular subcellular locations. This article includes an introduction to accessing the many suites of programs for analysis of protein structure, signatures of protein families, and consensus sequences that may be carried out on the internet.

L3 ANSWER 9 OF 15 MEDLINE DUPLICATE 7  
ACCESSION NUMBER: 2000097256 MEDLINE  
DOCUMENT NUMBER: 20097256 PubMed ID: 10631681  
TITLE: Protein consensus sequence motifs.  
AUTHOR: Aitken A  
CORPORATE SOURCE: Department of Biomedical Sciences (Biochemistry),  
University of Edinburgh, UK.. Alastair.Aitken@ed.ac.uk  
SOURCE: MOLECULAR BIOTECHNOLOGY, (1999 Oct) 12 (3) 241-53. Ref: 3  
Journal code: 9423533. ISSN: 1073-6085.  
PUB. COUNTRY: United States  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE).  
General Review; (REVIEW)  
(REVIEW, TUTORIAL)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals  
ENTRY MONTH: 200003  
ENTRY DATE: Entered STN: 20000314  
Last Updated on STN: 20000314  
Entered Medline: 20000302

[illegible]



1st & 2nd denotes  
time taken to a  
library

O/N - Under NLM  
means Overnight  
Service

FX - Means Faxed ( )